

&lt;!--StartFragment--&gt;ZCCHV\_RAT

ID ZCCHV\_RAT Reviewed; 776 AA.  
AC Q8K3Y6;  
DT 10-MAY-2004, integrated into UniProtKB/Swiss-Prot.  
DT 01-OCT-2002, sequence version 1.  
DT 25-NOV-2008, entry version 34.  
DE RecName: Full=Zinc finger CCCH-type antiviral protein 1;  
DE Short=Zinc finger antiviral protein;  
DE Short=rZAP;  
GN Name=Zc3havl; Synonyms=Zap;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidea; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [mRNA], FUNCTION, AND TISSUE SPECIFICITY.  
RX PubMed=12215647; DOI=10.1126/science.1074276;  
RA Gao G., Guo X., Goff S.P.;  
RT "Inhibition of retroviral RNA production by ZAP, a CCCH-type zinc  
RT finger protein.";  
RL Science 297:1703-1706 (2002).  
RN [2]  
RP PROTEIN SEQUENCE OF 227-238; 341-349; 359-371 AND 548-562, AND MASS  
RP SPECTROMETRY.  
RC STRAIN=Sprague-Dawley; TISSUE=Brain;  
RA Lubec G., Kang S.U., Lubec S.;  
RL Submitted (SEP-2007) to UniProtKB.  
RN [3]  
RP FUNCTION.  
RX PubMed=14557641; DOI=10.1128/JVI.77.21.11555-11562.2003;  
RA Bick M.J., Carroll J.W., Gao G., Goff S.P., Rice C.M., McDonald M.R.;  
RT "Expression of the zinc-finger antiviral protein inhibits alphavirus  
RT replication.";  
RL J. Virol. 77:11555-11562 (2003).  
RN [4]  
RP SUBCELLULAR LOCATION, NUCLEAR LOCALIZATION SIGNAL, AND NUCLEAR EXPORT  
RP SIGNAL.  
RX PubMed=15358138; DOI=10.1016/j.bbrc.2004.06.174;  
RA Liu L., Chen G., Ji X., Gao G.;  
RT "ZAP is a CRM1-dependent nucleocytoplasmic shuttling protein.";  
RL Biochem. Biophys. Res. Commun. 321:517-523 (2004).  
RN [5]  
RP RNA-BINDING.  
RX PubMed=15542630; DOI=10.1128/JVI.78.23.12781-12787.2004;  
RA Guo X., Carroll J.-W., McDonald M.R., Goff S.P., Gao G.;  
RT "The zinc finger antiviral protein directly binds to specific viral  
RT mRNAs through the CCCH zinc finger motifs.";  
RL J. Virol. 78:12781-12787 (2004).

RN [6]  
RP FUNCTION.  
RX PubMed=17182693; DOI=10.1128/JVI.01601-06;  
RA Mueller S., Moeller P., Bick M.J., Wurr S., Becker S., Guenther S.,  
RA Kuemmerer B.M.;  
RT "Inhibition of filovirus replication by the zinc finger antiviral  
RT protein.";  
RL J. Virol. 81:2391-2400 (2007).  
RN [7]  
RP FUNCTION, AND INTERACTION WITH EXOSC5.  
RX PubMed=17185417; DOI=10.1073/pnas.0607063104;  
RA Guo X., Ma J., Sun J., Gao G.;  
RT "The zinc-finger antiviral protein recruits the RNA processing exosome  
RT to degrade the target mRNA.";  
RL Proc. Natl. Acad. Sci. U.S.A. 104:151-156 (2007).  
CC -!- FUNCTION: Induces an innate immunity to viral infections by  
CC preventing the accumulation of viral RNAs in the cytoplasm. Seems  
CC to recruit the RNA processing exosome to degrade the target RNAs.  
CC Inhibits Moloney murine leukemia virus, alphavirus and filovirus  
CC replication.  
CC -!- SUBUNIT: Interacts with EXOSC5.  
CC -!- SUBCELLULAR LOCATION: Cytoplasm. Nucleus. Note=Localizes in the  
CC cytoplasm at steady state, but shuttles between nucleus and  
CC cytoplasm in a XPO1-dependent manner.  
CC -!- TISSUE SPECIFICITY: Expressed in the kidney and liver.  
CC -!- DOMAIN: The second and fourth zinc fingers are involved in binding  
CC to specific viral RNAs.  
CC -!- SIMILARITY: Contains 4 C3H1-type zinc fingers.  
CC -!- SIMILARITY: Contains 1 WWE domain.  
CC -----  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; AF521008; AAM75358.1; -; mRNA.  
DR UniGene; Rn.42053; -.  
DR PhosphoSite; Q8K3Y6; -.  
DR Ensembl; ENSRNOG00000013948; Rattus norvegicus.  
DR RGD; 628694; Zc3hav1.  
DR HOVERGEN; Q8K3Y6; -.  
DR GO; GO:0005737; C:cytoplasm; IEA:UniProtKB-KW.  
DR GO; GO:0005634; C:nucleus; IEA:UniProtKB-KW.  
DR GO; GO:0003723; F:RNA binding; IEA:UniProtKB-KW.  
DR GO; GO:0008270; F:zinc ion binding; IEA:InterPro.  
DR GO; GO:0009615; P:response to virus; IEA:UniProtKB-KW.  
DR InterPro; IPR004170; WWE.  
DR InterPro; IPR000571; Znf\_CCC.  
DR Pfam; PF00642; zf-CCCH; 1.  
DR PROSITE; PS50918; WWE; 1.  
DR PROSITE; PS50103; ZF\_C3H1; 2.

PE 1: Evidence at protein level;

KW Antiviral defense; Cytoplasm; Direct protein sequencing;

KW Metal-binding; Nucleus; Phosphoprotein; Repeat; RNA-binding; Zinc;

KW Zinc-finger.

FT CHAIN 1 776 Zinc finger CCCH-type antiviral protein 1.  
/FTId=PRO\_0000211344.

FT DOMAIN 671 758 WWE.

FT ZN\_FING 73 86 C3H1-type 1.

FT ZN\_FING 88 110 C3H1-type 2.

FT ZN\_FING 150 172 C3H1-type 3.

FT ZN\_FING 169 193 C3H1-type 4.

FT REGION 224 254 Binding to EXOSC5.

FT MOTIF 69 76 Nuclear localization signal.

FT MOTIF 284 291 Nuclear export signal.

FT MOTIF 405 406 Nuclear localization signal (Potential).

FT COMPIAS 343 348 Poly-Ser.

FT COMPIAS 415 418 Poly-Leu.

FT COMPIAS 533 536 Poly-Ser.

FT MOD\_RES 270 270 Phosphoserine (By similarity).

FT MOD\_RES 274 274 Phosphoserine (By similarity).

FT MOD\_RES 283 283 Phosphoserine (By similarity).

FT MOD\_RES 325 325 Phosphoserine (By similarity).

FT MOD\_RES 351 351 Phosphoserine (By similarity).

FT MOD\_RES 433 433 Phosphothreonine (By similarity).

FT MOD\_RES 459 459 Phosphoserine (By similarity).

FT MOD\_RES 501 501 Phosphotyrosine (By similarity).

SQ SEQUENCE 776 AA; 86771 MW; D13F61A9F8E5B552 CRC64;

Query Match 100.0%; Score 4129; DB 1; Length 776;  
Best Local Similarity 100.0%; Pred. No. 1.4e-257;  
Matches 776; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADPGVCCFITKILCAHGRMTLEELLGEIRLPEAQLYELLETAGPDRFVLLETGGQAGI 60  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 1 MADPGVCCFITKILCAHGRMTLEELLGEIRLPEAQLYELLETAGPDRFVLLETGGQAGI 60

Qy 61 TRSVVATTRARVCRKYCQRPCDSLHLCKLNLLGRCHYAQSQRLCKYSHDVLSEQNFQI 120  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 61 TRSVVATTRARVCRKYCQRPCDSLHLCKLNLLGRCHYAQSQRLCKYSHDVLSEQNFQI 120

Qy 121 LKNHELSGLNQEELACLLVQSDPFFLPEICKSYKGEGRKQTCGQPQPCERLHICEHFTRG 180  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 121 LKNHELSGLNQEELACLLVQSDPFFLPEICKSYKGEGRKQTCGQPQPCERLHICEHFTRG 180

Qy 181 NCSYLNCLRSNLMDRKVLTIMREHGLSPDVVQNIQDICNNKHARRNPPGTRAAPHRRG 240  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 181 NCSYLNCLRSNLMDRKVLTIMREHGLSPDVVQNIQDICNNKHARRNPPGTRAAPHRRG 240

Qy	241	GAHRDRSKSRDRLHNSLEFLSPVVSPLGSGPPSPDVTCKDSLEDVSDVTQKFYLGT	300
Db	241	GAHRDRSKSRDRLHNSLEFLSPVVSPLGSGPPSPDVTCKDSLEDVSDVTQKFYLGT	300
Qy	301	HDRAQLSPVSSKAAGVQGPSQMRASQEFSEDGNLDDIFSRNRSDSSSRASAAKVAQRNE	360
Db	301	HDRAQLSPVSSKAAGVQGPSQMRASQEFSEDGNLDDIFSRNRSDSSSRASAAKVAQRNE	360
Qy	361	AVAMKMGMEVKGKKEAPDIDRVPFLNSYIDGVTMEKASVSGIPGKKFTANDLENLLLND	420
Db	361	AVAMKMGMEVKGKKEAPDIDRVPFLNSYIDGVTMEKASVSGIPGKKFTANDLENLLLND	420
Qy	421	TWKNVAKPQDLQTTGRITDSGQDKAFLQNKYGGNPVWASASTHNAAPNGSSQIMDETPNVS	480
Db	421	TWKNVAKPQDLQTTGRITDSGQDKAFLQNKYGGNPVWASASTHNAAPNGSSQIMDETPNVS	480
Qy	481	KSSTSGFAIKPAIAGGKEAVYSGVQSPRSQVLAVPGEATTPVQSNRLPQSPLSSSHRAA	540
Db	481	KSSTSGFAIKPAIAGGKEAVYSGVQSPRSQVLAVPGEATTPVQSNRLPQSPLSSSHRAA	540
Qy	541	ASGSPGKNSTHTSVSPAIESSRMTSDPDEYLLRYILNPLFRMDNHGPKEICQDHLYKGQ	600
Db	541	ASGSPGKNSTHTSVSPAIESSRMTSDPDEYLLRYILNPLFRMDNHGPKEICQDHLYKGQ	600
Qy	601	QSHCDRSHFHLPYRWQMFVYTTWRDFQDMESIEQAYCDPHVELILIEHQINFQKMTCD	660
Db	601	QSHCDRSHFHLPYRWQMFVYTTWRDFQDMESIEQAYCDPHVELILIEHQINFQKMTCD	660
Qy	661	YPIRRLSTPSYEEKPLSAVFATKWIWYWKNEFNEYIQYGNESPGHTSSDINSAYLESFQ	720
Db	661	YPIRRLSTPSYEEKPLSAVFATKWIWYWKNEFNEYIQYGNESPGHTSSDINSAYLESFQ	720
Qy	721	SCPRGVLPFQAGSQKYELSFQGMIQTNIAASKTQRHVVRRPVFVSSNDVEQKRRGPE	776
Db	721	SCPRGVLPFQAGSQKYELSFQGMIQTNIAASKTQRHVVRRPVFVSSNDVEQKRRGPE	776

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